IN THE CLAIMS

Please amend the claims as indicated in the following listing of claims, which replaces all previous listings of claims.

1-5. (Canceled)

6. (Withdrawn) A method of detecting prostate cancer, the method comprising:

(a) detecting hybridization between a nucleic acid comprising at least 10 contiguous nucleotides of SEQ ID NO:1 and a PCGEM1 nucleic acid in a biological sample; and

(b) correlating the amount of the PCGEM1 nucleic acid in the biological sample with the presence of prostate cancer.

7. (Withdrawn) The method according to claim 6, further comprising before detecting hybridization:

(a) isolating RNA from the biological sample; and

(b) amplifying the PCGEM1 nucleic acid.

8. (Withdrawn) The method according to claim 7, wherein the PCGEM1 nucleic acid is amplified with at least two nucleotide sequences selected from SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO:13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, and SEQ ID NO: 22.

9. (Withdrawn) The method according to claim 8, wherein the at least two nucleotide sequences are SEQ ID NO:15 and SEQ ID NO:22.

10. (Withdrawn) A method according to claim 6, wherein the biological sample is selected from blood, urine, and prostate tissue.

11. (Withdrawn) The method according to claim 10, wherein the biological sample is blood.

12-21. (Canceled)

22. (Currently Amended) A method of detecting a PCGEM1 nucleic acid in a biological sample comprising ~~intact~~ cells, comprising:

combining the biological sample with a nucleic acid comprising at least 10 contiguous nucleotides of SEQ ID NO:1 under hybridizing conditions of moderate stringency; and

detecting hybridization between the nucleic acid comprising at least 10 contiguous nucleotides of SEQ ID NO:1 and the PCGEM1 nucleic acid in the biological sample, wherein hybridization indicates the presence of the PCGEM1 nucleic acid in the biological sample.

23. (Previously Presented) The method of claim 22, further comprising a step of amplifying the PCGEM1 nucleic acid before combining the biological sample with the nucleic acid comprising at least 10 contiguous nucleotides of SEQ ID NO: 1.

24. (Previously Presented) A method according to claim 22, wherein the biological sample is selected from blood, urine, and prostate tissue.

25. (Previously Presented) The method of claim 22, wherein the biological sample is prostate tissue.

26. (Previously Presented) The method of claim 22, wherein the biological sample is blood.

27. (Previously Presented) The method of claim 22, wherein the nucleic acid comprises at least about 17 contiguous nucleotides of SEQ ID NO:1.

28. (Previously Presented) The method according to claim 22, wherein the nucleic acid comprises at least 20 nucleic acids of SEQ ID NO:1.

29. (Previously Presented) The method according to claim 22, wherein the nucleic acid comprises at least 30 nucleic acids of SEQ ID NO:1.

30. (Previously Presented) The method according to claim 22, wherein the nucleic acid comprises at least 60 nucleic acids of SEQ ID NO:1.

31. (Withdrawn) The method of claim 6, wherein the nucleic acid comprises at least about 17 contiguous nucleotides of SEQ ID NO:1.

32. (Withdrawn) The method according to claim 6, wherein the nucleic acid comprises at least 20 contiguous nucleic acids of SEQ ID NO:1.

33. (Withdrawn) The method according to claim 6, wherein the nucleic acid comprises at least 30 contiguous nucleic acids of SEQ ID NO:1.

34. (Withdrawn) The method according to claim 6, wherein the nucleic acid comprises at least 60 contiguous nucleic acids of SEQ ID NO: 1.

35. (Withdrawn) The method according to claim 10, wherein the biological sample is prostate tissue.